Immediate Early (IE) Gene Expression

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

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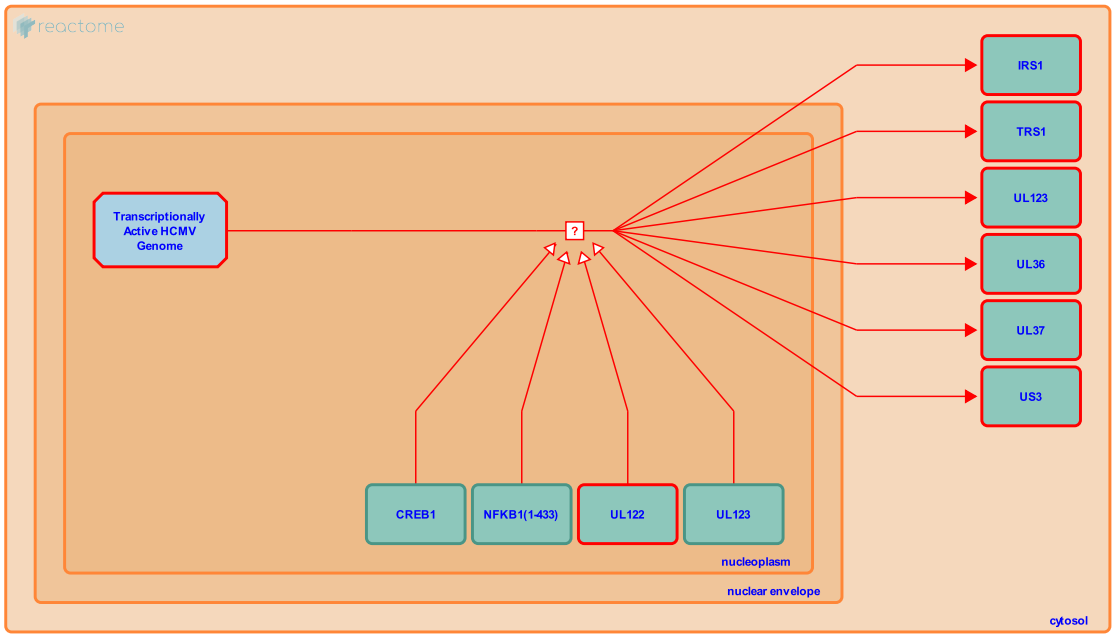
Stable identifier: R-HSA-9621073

Type: uncertain

Compartments: nucleoplasm

Diseases: disease by infectious agent



Once the HCMV genome is delivered to the nucleus, IE gene expression ensues. RNA pol II transcription machinery transcribes IE as well as all other protein-coding and noncoding RNAs made from the HCMV genome. Regulation of viral gene expression occurs via two broad strategies: (1) viral as well as cellular factors that directly influence the transcription machinery by binding to promoter/enhancer elements directly (transcription factors) or through interactions with other proteins (adaptors) (2) viral factors that alter chromatin remodeling by regulating the opposing activities of histone acetyl transferases (HATs) acting together with demethylases and histone deacetylases (HDACs) and methylases. HDAC-dependent repression of viral IE gene expression, in particular, is a cell-intrinsic host defense mechanism that must be defused before productive replication can ensue. Epigenetic regulation is important in permissive cells, even though the viral genome does not take on a recognizable chromatin structure, and also during latency, where viral genomes take on an organized chromatin arrangement and viral HDAC inhibitors can drive reactivation.

Literature references

Knipe, DM., Howley, PM. (2013). Chapter 62 - Cytomegaloviruses, Fields Virology. *Lippincott Williams & Wilkins*.

Editions

2019-10-18	Reviewed	Streblow, DN., Caposio, P.